

# SEQUENCE LISTING

<110> GOODNOW, Jr., Robert Alan  
MARK, David Fu-Chi  
MARTIN, Mitchell Lee  
ROSINSKI, James Andrew

<120> Sequence #115 as a target for identifying weight modulating compounds

<130> 21366

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<150> US 60/436,375

<151> 2002-12-23

<160> 6

<170> PatentIn version 3.2

<210> 1

<211> 1011

<212> DNA

<213> Mus musculus

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<221> GPCR #115

<222> (1)..(1011)

<223> CHR7-36867

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<210> 2
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<213> Mus musculus

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Gly Val Ser Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Leu Leu His
          20          25          30

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Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu
          35          40          45

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Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu
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Ala Gly Val Val Ala Gln Arg Gln Pro Ala Gly Asp Arg Leu Cys Arg
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Ser Tyr Arg Ala Lys Met Arg Leu Arg Asp Ala Ala Leu Met Val Ala  
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Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Ala Ala Leu Ala Leu  
130 135 140

Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser  
145 150 155 160

Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Gly Ala Phe  
165 170 175

His Ala Leu Ser Phe Leu Leu Ser Phe Val Val Leu Cys Cys Thr Tyr  
180 185 190

Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val  
195 200 205

Ile Thr Met Gln Thr Leu Val Leu Leu Val Asp Leu His Pro Ser Val  
210 215 220

Arg Glu Arg Cys Leu Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr  
225 230 235 240

Lys Lys Ile Ser Thr Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro  
245 250 255

Tyr Val Ile Thr Arg Leu Val Glu Leu Phe Ser Thr Val Pro Ile Gly  
260 265 270

Ser His Trp Gly Val Leu Ser Lys Cys Leu Ala Tyr Ser Lys Ala Ala  
275 280 285

Ser Asp Pro Phe Val Tyr Ser Leu Leu Arg His Gln Tyr Arg Lys Ser  
290 295 300

Cys Lys Glu Ile Leu Asn Arg Leu Leu His Arg Arg Ser Ile His Ser  
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Ser Gly Leu Thr Gly Asp Ser His Ser Gln Asn Ile Leu Pro Val Ser  
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 <213> Rattus norvegicus

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<220>  
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 20 25 30

Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu  
 35 40 45

Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu  
 50 55 60

Ala Gly Val Val Ala Gln Arg Gln Pro Ala Gly Asp Arg Leu Cys Arg  
 65 70 75 80

Leu Ala Ala Phe Leu Asp Thr Phe Leu Ala Ala Asn Ser Met Leu Ser  
 85 90 95

Met Ala Ala Leu Ser Ile Asp Arg Trp Val Ala Val Val Phe Pro Leu

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Ser Tyr Arg Ala Lys Met Arg Leu Arg Asp Ala Ala Phe Met Val Ala		
115	120	125
Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Thr Ala Leu Ala Leu		
130	135	140
Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser		
145	150	155
Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Ser Ala Phe		
165	170	175
His Ala Leu Ser Phe Leu Leu Ser Phe Ile Val Leu Cys Phe Thr Tyr		
180	185	190
Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val		
195	200	205
Ile Thr Met Gln Thr Leu Val Leu Leu Val Asp Ile His Pro Ser Val		
210	215	220
Arg Glu Arg Cys Leu Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr		
225	230	235
Lys Lys Ile Ser Thr Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro		
245	250	255
Tyr Val Ile Thr Arg Leu Val Glu Leu Phe Ser Thr Ala Pro Ile Asp		
260	265	270
Ser His Trp Gly Val Leu Ser Lys Cys Leu Ala Tyr Ser Lys Ala Ala		
275	280	285
Ser Asp Pro Phe Val Tyr Ser Leu Leu Arg His Gln Tyr Arg Arg Ser		
290	295	300
Cys Lys Glu Leu Leu Asn Arg Ile Phe Asn Arg Arg Ser Ile His Ser		

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Val Gly Leu Thr Gly Asp Ser His Ser Gln Asn Ile Leu Pro Val Ser  
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Glu

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 <212> DNA  
 <213> Homo sapiens

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 <223> AJ505757

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20 25 30

Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu  
35 40 45

Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu  
50 55 60

Ala Gly Val Val Ala Gln Arg Gln Pro Ala Gly Asp Arg Leu Cys Arg  
65 70 75 80

Leu Ala Ala Phe Leu Asp Thr Phe Leu Ala Ala Asn Ser Met Leu Ser  
85 90 95

Met Ala Ala Leu Ser Ile Asp Arg Trp Val Ala Val Val Phe Pro Leu  
100 105 110

Ser Tyr Arg Ala Lys Met Arg Leu Arg Asp Ala Ala Leu Met Val Ala  
115 120 125

Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Ala Ala Leu Ala Leu  
130 135 140



Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser  
 145 150 155 160

Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Gly Ala Phe  
 165 170 175

His Ala Leu Ser Phe Leu Leu Ser Phe Val Val Leu Cys Cys Thr Tyr  
 180 185 190

Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val  
 195 200 205

Ile Thr Met Gln Thr Leu Val Leu Leu Val Asp Leu His Pro Ser Val  
 210 215 220

Arg Glu Arg Cys Leu Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr  
 225 230 235 240

Lys Lys Ile Ser Thr Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro  
 245 250 255

Tyr Val Ile Thr Arg Leu Val Glu Leu Phe Ser Thr Val Pro Ile Gly  
 260 265 270

Ser His Trp Gly Val Leu Ser Lys Cys Leu Ala Tyr Ser Lys Ala Ala  
 275 280 285

Ser Asp Pro Phe Val Tyr Ser Leu Leu Arg His Gln Tyr Arg Lys Ser  
 290 295 300

Cys Lys Glu Ile Leu Asn Arg Leu Leu His Arg Arg Ser Ile His Ser  
 305 310 315 320

Ser Gly Leu Thr Gly Asp Ser His Ser Gln Asn Ile Leu Pro Val Ser  
 325 330 335

Glu